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FILE 'REGISTRY' ENTERED AT 17:10:57 ON 02 SEP 2008
              EXP ASPARAGINE/CN
             2 S E3
T.1
    FILE 'HCAPLUS' ENTERED AT 17:11:13 ON 02 SEP 2008
        18606 S L1
L2
L3
             1 S DISIALOUNDECA?
L4
        228020 S FATTY ACID
L5
            0 S L2 AND L3 AND L4
L6
           253 S L2 AND L4
L7
        48927 S SIAL?
L8
            1 S L6 AND L7
L9
        49425 S SIAL? OR DISIAL?
            1 S L2 AND L4 AND L9
L10
          167 S L2 AND L9
L11
          134 S L11 AND (PY<2004 OR AY<2004 OR PRY<2004)
L12
L13
       138568 S AMIDE
            2 S L12 AND L13
L14
    FILE 'HCAPLUS' ENTERED AT 17:29:03 ON 02 SEP 2008
L15
    4664798 S ACID
L16
            92 S L12 AND L15
    FILE 'HCAPLUS' ENTERED AT 17:30:17 ON 02 SEP 2008
L17
     157350 S CAPRIC OR LAURIC OR MYRISTIC OR PALMITIC OR STEARIC OR ARACHI
L18
             0 S L16 AND L17
    FILE 'HCAPLUS' ENTERED AT 17:30:38 ON 02 SEP 2008
      0 S L12 AND L17
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L19

=> file registry COST IN U.S. DOLLARS

SINCE FILE TOTAL ENTRY SESSION FULL ESTIMATED COST 0.21 0.21

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1 SEP 2008 HIGHEST RN 1045602-82-1 STRUCTURE FILE UPDATES: DICTIONARY FILE UPDATES: 1 SEP 2008 HIGHEST RN 1045602-82-1

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TSCA INFORMATION NOW CURRENT THROUGH July 5, 2008.

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http://www.cas.org/support/stngen/stndoc/properties.html

=> exp asparagine/cn

E1	1	ASPARAGINASE/GLUTAMINASE (SALINISPORA TROPICA STRAIN CNB-440)/CN
E2	1	ASPARAGINASE/GLUTAMINASE (THIOMICROSPIRA CRUNOGENA STRAIN XC L-2)/CN
E3	2>	ASPARAGINE/CN
E4	1	ASPARAGINE (GLUTAMINE) SYNTHETASE/CN
E5	1	ASPARAGINE TRNA LIGASE (PLASMODIUM FALCIPARUM STRAIN 3D7
		GENE PFB0525W)/CN
E6	1	ASPARAGINE ACID/CN
E7	1	ASPARAGINE AMIDE/CN
E8	1	ASPARAGINE AMIDE HYDROBROMIDE/CN
E9	1	ASPARAGINE AMIDOHYDROLASE (DIROFILARIA IMMITIS CLONE L3MC4)/
		CN
E10	1	ASPARAGINE AMINOTRANSFERASE/CN
E11	1	ASPARAGINE ANHYDRIDE/CN
E12	1	ASPARAGINE BENZYL ESTER HYDROCHLORIDE/CN

=> s e3

L12 ASPARAGINE/CN

=> file hcaplus

COST IN U.S. DOLLARS SINCE FILE TOTAL ENTRY SESSION FULL ESTIMATED COST 5.61 5.82

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=> s 11 18606 L1 => s disialoundeca? 1 DISIALOUNDECA? => s fatty acid 408232 FATTY 4664798 ACID 228020 FATTY ACID T. 4 (FATTY(W)ACID)  $\Rightarrow$  s 12 and 13 and 14 L50 L2 AND L3 AND L4 => s 12 and 14 253 L2 AND L4 => s sial? L7 48927 SIAL? => s 16 and 17 1 L6 AND L7 1.8 => d 18 ti absbib 'ABSBIB' IS NOT A VALID FORMAT FOR FILE 'HCAPLUS' The following are valid formats: ABS ---- GI and AB ALL ----- BIB, AB, IND, RE APPS ----- AI, PRAI BIB ----- AN, plus Bibliographic Data and PI table (default) CAN ----- List of CA abstract numbers without answer numbers

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DMAX ----- MAX, delimited for post-processing

DALL ----- ALL, delimited (end of each field identified)

FAM ----- AN, PI and PRAI in table, plus Patent Family data

CLASS ----- IPC, NCL, ECLA, FTERM

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IND ----- Indexing data
IPC ----- International Patent Classifications
\mbox{MAX} ----- ALL, plus Patent FAM, RE
PATS ----- PI, SO
SAM ----- CC, SX, TI, ST, IT
SCAN ----- CC, SX, TI, ST, IT (random display, no answer numbers;
             SCAN must be entered on the same line as the DISPLAY,
             e.g., D SCAN or DISPLAY SCAN)
STD ----- BIB, CLASS
IABS ----- ABS, indented with text labels
IALL ----- ALL, indented with text labels
IBIB ----- BIB, indented with text labels
{\tt IMAX} ----- {\tt MAX}\textsc{,} indented with text labels
ISTD ----- STD, indented with text labels
OBIB ----- AN, plus Bibliographic Data (original)
OIBIB ----- OBIB, indented with text labels
SBIB ----- BIB, no citations
SIBIB ----- IBIB, no citations
HIT ----- Fields containing hit terms
HITIND ----- IC, ICA, ICI, NCL, CC and index field (ST and IT)
             containing hit terms
HITRN ----- HIT RN and its text modification
HITSTR ----- HIT RN, its text modification, its CA index name, and
             its structure diagram
HITSEQ ----- HIT RN, its text modification, its CA index name, its
             structure diagram, plus NTE and SEQ fields
FHITSTR ---- First HIT RN, its text modification, its CA index name, and
             its structure diagram
FHITSEQ ---- First HIT RN, its text modification, its CA index name, its
             structure diagram, plus NTE and SEQ fields
KWIC ----- Hit term plus 20 words on either side
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FBIB ----- AN, BIB, plus Patent FAM

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OCC ----- Number of occurrence of hit term and field in which it occurs

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- L8 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2008 ACS on STN
- TI The glycan structure of albumin Redhill, a glycosylated variant of human serum albumin
- AB Although human serum albumin is synthesized without carbohydrate, glycosylated variants of the protein can be found. We have determined the structure of the glycan bound to the double-mutant albumin Redhill (-1 Arg, 320 Ala-Thr). The oligosaccharide was released from the protein using anhydrous hydrazine, and its structure was investigated using neuraminidase and a reagent array anal. method, which is based on the use of specific exoglycosidases. The glycan was shown to be a disialylated biantennary complex type oligosaccharide N-linked to 318 Asn. However, a

minor part (11 mol%) of the glycan was without sialic acid. The structure is principally the same as that of glycans bound to two other types of glycosylated albumin variants. Glycosylation can affect, for example, the fatty acid binding properties of albumin. Taking the present information into account, it is apparent that different effects on binding are caused not by different glycan structures but by different locations of attachment, with the possible addition of local conformational changes in the protein mol.

- ΑN 2001:884107 HCAPLUS <<LOGINID::20080902>>
- 136:179567 DN
- The glycan structure of albumin Redhill, a glycosylated variant of human ΤI serum albumin
- ΑU Kragh-Hansen, Ulrich; Donaldson, David; Jensen, Poul Henning
- CS Department of Medical Biochemistry, University of Aarhus, Aarhus, DK-8000, Den.
- SO Biochimica et Biophysica Acta, Protein Structure and Molecular Enzymology (2001), 1550(1), 20-26CODEN: BBAEDZ; ISSN: 0167-4838
- ΡВ Elsevier B.V.
- DT Journal
- T.A English
- RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

## => d his

(FILE 'HOME' ENTERED AT 17:10:48 ON 02 SEP 2008)

FILE 'REGISTRY' ENTERED AT 17:10:57 ON 02 SEP 2008 EXP ASPARAGINE/CN

2 S E3 T.1

FILE 'HCAPLUS' ENTERED AT 17:11:13 ON 02 SEP 2008

L2 18606 S L1

L3 1 S DISIALOUNDECA?

228020 S FATTY ACID L4

L5 0 S L2 AND L3 AND L4

L6 253 S L2 AND L4 L7

48927 S SIAL?

1 S L6 AND L7 L8

=> log hold

COST IN U.S. DOLLARS SINCE FILE TOTAL ENTRY SESSION FULL ESTIMATED COST 8.29 14.11

SINCE FILE DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) TOTAL ENTRY SESSION CA SUBSCRIBER PRICE -0.80-0.80

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PASSWORD:
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=> s sial? or disial? 48927 SIAL? 1174 DISIAL? L9 49425 SIAL? OR DISIAL?

=> s 12 and 19 L11 167 L2 AND L9

=> s l11 and (PY<2004 or AY<2004 or PRY<2004) 24009542 PY<2004 4785121 AY<2004 4256259 PRY<2004

L12 134 L11 AND (PY<2004 OR AY<2004 OR PRY<2004)

=> s amide

L13 138568 AMIDE

=> s 112 and 114 L14 NOT FOUND The L-number enter

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=> d 114 1-2 ti abs bib

L14 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2008 ACS on STN

TI Characterization of N-linked oligosaccharides attached to recombinant human antithrombin expressed in the yeast Pichia pastoris

AB We studied the structures of four N-linked oligosaccharide chains of the recombinant human antithrombin (rAT) expressed in the yeast Pichia pastoris. RAT was fully glycosylated at Asn 96 and Asn 155, whereas the glycosylation on Asn 135 and Asn 192 was partial. The glycosylation level on Asn 135 was only 12% and this reduction is assumed to be one of the reasons for a higher heparin-binding affinity of rAT than plasma-derived human antithrombin (pAT). In order to determine the sizes and electrostatic charges of the N-linked oligosaccharides, rAT was treated with PNGase F, and the reduced ends were labeled by pyridylamination followed by anal. using anion exchange and amide adsorption columns. The N-linked oligosaccharides were 78% neutral and 22% phosphomannosylated. The neutral oligosaccharides were thought to be Man9-12GlcNAc2 as their major

components. The phosphomannosylated oligosaccharides were then subjected to mild acid hydrolysis and/or digestion with alkaline phosphatase, and their charge shifts were analyzed by the affinity to an anion exchange column. Among phosphomannosylated oligosaccharides, monophosphate diester type was predominant, whereas neg. charged diphosphate diester and monophosphate monoester types were minor components. The mannose residues at the non-reducing end(s) of Man9-12GlcNAc2 were phosphomannosylated or phosphorylated and these are the major components. Because rAT is less neg. charged than pAT, which has disially biantennary N-glycans, it might be less repulsive to pentasaccharide-bearing anticoagulantly active heparan sulfate proteoglycan mols. exposed on the surface of the damaged vascular vessels.

- AN 2002:813772 HCAPLUS <<LOGINID::20080902>>
- DN 138:51890
- TI Characterization of N-linked oligosaccharides attached to recombinant human antithrombin expressed in the yeast Pichia pastoris
- AU Hirose, Masaaki; Kameyama, Shoju; Ohi, Hideyuki
- CS Protein Research Laboratory, Pharmaceutical Research Division, Mitsubishi Pharma Corporation, Osaka, 573-1153, Japan
- SO Yeast (2002), 19(14), 1191-1202 CODEN: YESTE3; ISSN: 0749-503X
- PB John Wiley & Sons Ltd.
- DT Journal
- LA English
- RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT
- L14 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2008 ACS on STN
- TI Oligosaccharide units of rabbit immunoglobulin G. Multiple carbohydrate attachment sites
- AB The carbohydrate structure of rabbit immunoglobulin G isolated from pooled serums was determined Amino sugar anal. of fragments of the mol. showed 3 oligosaccharides located at separate sites on the H-chain and the corresponding glycopeptides were isolated. The average composition of the Cl-oligosaccharide, present on .apprx.15% of the H-chains, was 2 glucosamine, 2 mannose, and 1 galactose residues; the carbohydrate was coupled through the amide group of asparagine in a peptide containing asparagine, glycine, and threonine within the Fd fragment of the mol. The average composition of the C2-oligosaccharide, present on .apprx.40%

of
the H-chains, was 1 galactosamine, 1 galactose, and either 1 or 2
sialic acid residues; it was attached glycosidically to the OH
group of threonine in a peptide Ser-Lys-Pro-Thr-Cys-Pro-Pro-Pro-Glu-Leu in
the hinge region of the mol. The average composition of the

C3-oligosaccharide,
present in all the H-chains, was 5 glucosamine, 2 galactose, 5 mannose, 1
fucose, and 1 sialic acid residue; it was linked through the
amide group of asparagine in a peptide Gln-Gln-Phe-Asn-Ser-Thr-IleArg within the Fc fragment of the mol.

- AN 1972:459855 HCAPLUS <<LOGINID::20080902>>
- DN 77:59855
- OREF 77:9913a,9916a
- TI Oligosaccharide units of rabbit immunoglobulin G. Multiple carbohydrate attachment sites
- AU Fanger, M. W.; Smyth, D. G.
- CS Natl. Inst. Med. Res., London, UK
- SO Biochemical Journal (1972), 127(5), 757-65 CODEN: BIJOAK; ISSN: 0264-6021
- DT Journal
- LA English

=> file stnguise
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=> file hcaplus

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=> s acid L15 4664798 ACID

=> s 112 and 115

L16 92 L12 AND L15

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ENTRY SESSION
FULL ESTIMATED COST
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28.06

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ENTRY SESSION

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 $\Rightarrow$  s capric or lauric or myristic or palmitic or stearic or arachic or behenic or oleic

6255 CAPRIC
20076 LAURIC
16240 MYRISTIC
42544 PALMITIC
76090 STEARIC
547 ARACHIC
5138 BEHENIC

71101 OLEIC

L17 157350 CAPRIC OR LAURIC OR MYRISTIC OR PALMITIC OR STEARIC OR ARACHIC OR BEHENIC OR OLEIC

=> s 116 and 117

L18 0 L16 AND L17

=> file stnguide

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=> s 112 and 117

L19 0 L12 AND L17